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Search: protein - protein database search, using Smith-Waterman algorithm  
Run on: Sat May 13 08:59:53 2000; Maspar time 4.30 Seconds  
302,703 Million cell updates/sec  
Tabular output not generated.

Title: >US-09-331-631-24  
Description: (31-85) from US09331631.pep  
Perfect Score: 425  
Sequence: 1 DEDDRGGSHLQCCVQRCRQ.....DDQOQHGHEQEEQGRG 55

Scoring table:  
PAM 150  
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq35  
1:geneseqp

Statistics: Mean 23.678; Variance 101.499; scale 0.235

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	425	100.0	637	1	W62837	Hordeum vulgare antim	2.03e-31
2	174	40.9	593	1	W62835	Zea mays antimicrobial	1.55e-07
3	131	30.8	590	1	W62832	Gossypium hirsutum ant	1.08e-03
4	129	30.4	666	1	W62828	Macadamia integrifolia	1.61e-03
5	129	30.4	666	1	W62829	Macadamia integrifolia	1.61e-03
6	105	24.7	625	1	W62830	Macadamia integrifolia	1.83e-01
7	105	24.7	898	1	W31853	Mycobacterium tubercul	1.83e-01
8	95	22.4	409	1	W90342	G. max truncated SBP2	1.24e+00
9	95	22.4	489	1	W90341	G. max SBP2 protein.	1.24e+00
10	89	20.9	525	1	W62831	Theobroma cacao antim	3.82e+00
11	89	20.9	566	1	R20181	Sequence encoded by 67	3.82e+00
12	85	20.0	450	1	W46606	Tyrosine kinase associ	8.02e+00
13	84	19.8	97	1	W59348	Human ERB2 extracellu	9.64e+00
14	84	19.8	444	1	W90340	G. max truncated SBP1	9.64e+00
15	84	19.8	524	1	W90339	G. max SBP1 protein.	9.64e+00
16	84	19.8	624	1	R08222	Extracellular portion	9.64e+00
17	84	19.8	782	1	W19764	Her2-GM-CSF immunostim	9.64e+00
18	84	19.8	1255	1	W01111	Human HER-2/neu oncoge	9.64e+00
19	84	19.8	1255	1	W01111	HER-2/neu protein.	9.64e+00
20	83	19.5	626	1	W22150	Peanut allergen Ara hi	1.16e+01
21	83	19.5	1829	1	Y07242	Actin-filament binding	1.16e+01
22	82	19.3	539	1	W33628	Yeast transcriptional	1.39e+01
23	80	18.8	374	1	W97834	Human Fc receptor I.	2.00e+01

24	77	18.1	614	1	W22149	Peanut allergen Ara hi	3.43e+01
25	77	18.1	614	1	W62834	Arachis hypogaea antim	3.43e+01
26	77	18.1	1382	1	W31867	Human metastasis-assoc	3.43e+01
27	77	18.1	1433	1	R39568	Sequence of c-erbB-2 t	3.43e+01
28	76	17.9	150	1	P70058	Human epidermal growth	4.10e+01
29	76	17.9	405	1	W33737	Epidermal growth facto	4.10e+01
30	76	17.9	451	1	R27721	Mouse perforin C-termi	4.10e+01
31	76	17.9	509	1	R38210	Mouse perforin C-termi	4.10e+01
32	76	17.9	529	1	R38209	ID1D3D4 EGF receptor t	4.10e+01
33	76	17.9	554	1	R05271	LD1D2D3. Apat EGF recep	4.10e+01
34	75	17.6	288	1	W45748	Amino acid sequence of	4.90e+01
35	74	17.4	541	1	W37148	Human cardiac troponin	5.85e+01
36	74	17.4	709	1	P91934	Mammalian Ena (Mena).	5.85e+01
37	74	17.4	783	1	W37151	Mouse neural Mena+ pro	5.85e+01
38	74	17.4	787	1	W37152	Mouse neural Mena+ pr	5.85e+01
39	74	17.4	802	1	W37153	Mouse neural Mena+ p	5.85e+01
40	73	17.2	193	1	W30750	Partial human YTS21 ge	6.98e+01
41	73	17.2	404	1	R27284	Sequence encoded by th	6.98e+01
42	73	17.2	712	1	W30749	Rat YTS21 gene product	6.98e+01
43	73	17.2	1529	1	R97985	CORC potassium channel	6.98e+01
44	72	16.9	76	1	R22394	Antigen tc-10a.	8.32e+01
45	72	16.9	340	1	W81594	Protein encoded by hum	8.32e+01

## ALIGNMENTS

RESULT	1	4
ID	W62837 standard; Protein: 637 AA.	
AC	W62837	
DT	27-OCT-1998 (first entry)	
DE	Hordeum vulgare antimicrobial protein.	
KW	antimicrobial protein; infestation; control.	
OS	Hordeum vulgare.	
PD	W09827805-A1.	
PN	02-JUL-1998.	
PE	22-DEC-1997; AU0874.	
PR	20-DEC-1996; AU-004275.	
PA	(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.	
PI	Bower NJ, Goulter KC, Green JL, Manners JM, Marcus JP;	
DR	WPI: 98-372729/32.	
PT	Novel anti-microbial protein from e.g. Macadamia integrifolia -	
PT	useful for controlling microbial infestations of plants or mammals	
PS	Claim 1; Page 60-62; 96pp; English.	
CC	The sequence is that of an antimicrobial protein which can	
CC	be used to control microbial infestations in plants and mammalian	
CC	animals.	
CC	Sequence 637 AA.	
QY	31 DEDDRGGSHLQCCVQRCRQERPRYSHARCVCRRDQOQHGHEEQGRG 85	
DB	31 DEDDRGGSHLQCCVQRCRQERPRYSHARCVCRRDQOQHGHEEQGRG 85	
QY	31 DEDDRGGSHLQCCVQRCRQERPRYSHARCVCRRDQOQHGHEEQGRG 85	
RESULT	2	
ID	W62835 standard; Protein: 593 AA.	
AC	W62835	
DT	27-OCT-1998 (first entry)	
DE	Zea mays antimicrobial protein.	
KW	antimicrobial protein; infestation; control.	
OS	Zea mays.	
PD	W09827805-A1.	
PN	02-JUL-1998.	
PE	22-DEC-1997; AU0874.	
PR	20-DEC-1996; AU-004275.	
PA	(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.	
PI	Bower NJ, Goulter KC, Green JL, Manners JM, Marcus JP;	
DR	WPI: 98-372729/32.	
PT	Novel anti-microbial protein from e.g. Macadamia integrifolia -	
PT	useful for controlling microbial infestations of plants or mammals	



SQ Sequence 625 AA;

Query Match 24.7%; Score 105; DB 1; Length 625;  
Best Local Similarity 31.1%; Pred. No. 1.83e-01;  
Matches 14; Conservative 16; Mismatches 12; Indels 3; Gaps 2;

DB 141 EGNKRPDQOREYEDCRHRCQDEPRL-QYCCQRQCEQQRGR 184  
QY 31 DEDRRRGH--SLQCCVQRCERRPRYSNARCVOECRDDQOGR 73

RESULT 7  
ID W31853 standard; Protein; 898 AA.  
AC W31853;  
DT 27-APR-1998 (first entry)  
DE Mycobacterium tuberculosis 77 kDa protein.  
KM Tuberculosis; mycobacteria; infection; diagnosis;  
KW antimycobacterial; antibiotic; vaccine.  
OS Mycobacterium tuberculosis.  
PN W09741252-A2.  
PD 06-NOV-1997.  
PF 18-APR-1997; E01973.  
PR 29-APR-1996; DE-017184.  
PA (GBFR) GBF GES BIOTECH FORSCHUNG GMBH.  
PI Espitia C, Honisch C, Moreno C, Singh M;  
DR WPI; 97-549750/50.  
DR N-PSDB; T93610.  
PT New DNA and related proteins or RNA derived from M. tuberculosis -  
PT used for diagnosis of mycobacterial infections, monitoring  
PT vaccination and development of anti-mycobacterial agents  
PS Claim 7; Fig 14, 55pp: English.  
CC This novel 77 kDa protein is encoded by an open reading frame of  
CC a Mycobacterium tuberculosis DNA fragment (see T93610) containing  
CC polymorphic GC-rich sequences. It is highly enriched in glycine  
CC and may be a cell wall protein. Novel M. tuberculosis proteins  
CC (see W31851-57) are claimed. These can be produced as recombinant  
CC proteins, especially in bacterial, yeast, fungal or higher  
CC eukaryote host cells, and used for diagnosing tuberculosis and  
CC other mycobacterial infections in humans or animals. The claimed  
CC proteins can also be used for epidemiological studies, for  
CC monitoring vaccination, and for the development of vaccines and  
CC anti-mycobacterial drugs.  
SQ Sequence 898 AA;

Query Match 24.7%; Score 105; DB 1; Length 898;  
Best Local Similarity 31.6%; Pred. No. 1.83e-01;  
Matches 12; Conservative 15; Mismatches 10; Indels 1; Gaps 1;

DB 821 CRRVWRRYRRORWCRORADRRORRRORRQSGHAR 858  
QY 48 CROERPRYSNAR-CVOECRDDQOGRHNEDEEGGRGR 84

RESULT 8  
ID W90342 standard; Protein; 409 AA.  
AC W90342;  
DT 24-MAY-1999 (first entry)  
DE G. max truncated SBP2 protein.  
KM SBP1: sucrose binding protein; SBP2: sucrose uptake; transgenic plant;  
KW seed; carbohydrate content; soybean.  
OS Glycine max.  
PN W09853086-A1.  
PD 26-NOV-1998.  
PF 21-MAY-1998; U10465.  
PR 23-MAY-1997; US-047568.  
PA (UNIV) UNIV WASHINGTON STATE RES FOUND.  
PI Chao WS, Grimes HD;  
DR WPI; 99-070155/06.  
PT New modified plant sucrose binding proteins - used to develop  
PT transgenic plants which can have enhanced or decreased sucrose  
PT uptake activity in developing seeds  
PS Claim 7; Page 39-40; 58pp: English.  
CC This sequence represents a novel sucrose binding protein, SBP2 isolated

CC from Glycine max. This protein is used in a method resulting in the  
CC production of a modified plant sucrose binding protein (SBP) which has a  
CC modified amino acid sequence compared to a corresponding wild-type SBP,  
CC and where expression of the modified SBP in a yeast assay system confers  
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.  
CC The products of the invention can be used for producing transgenic plants  
CC which have modified sucrose uptake activity, particularly in developing  
CC seeds. Enhanced sucrose uptake activity in developing seeds may be  
CC desirable where it is an advantage to increase the carbohydrate content  
CC of the seed (e.g. where the seed is the primary plant material harvested,  
CC seeds might be desirable where the vegetative material of the plant is  
CC harvested. The SBP regulatory regions confer specific or enhanced  
CC expression in developing seeds and so may be used to express any  
CC transgene in developing seeds.  
SQ Sequence 489 AA;

Query Match 22.4%; Score 95; DB 1; Length 489;  
Best Local Similarity 36.2%; Pred. No. 1.24e+00;  
Matches 17; Conservative 11; Mismatches 13; Indels 6; Gaps 5;

DB 39 LVTCKHQCQOQR-QYTESDKRTCLQOC-DSMKOE-REKQVEETREK 82  
QY 41 LQCCVQRCERRPRYSNAR--R-CVOECRDDQOGRHNEDEEGGRGR 84

RESULT 9  
ID W90341 standard; Protein; 489 AA.  
AC W90341;  
DT 24-MAY-1999 (first entry)  
DE G. max SBP2 protein.  
KM SBP1: sucrose binding protein; SBP2: sucrose uptake; transgenic plant;  
KW seed; carbohydrate content; soybean.  
OS Glycine max.  
PN W09853086-A1.  
PD 26-NOV-1998.  
PF 21-MAY-1998; U10465.  
PR 22-MAY-1997; US-047568.  
PA (UNIV) UNIV WASHINGTON STATE RES FOUND.  
PI Chao WS, Grimes HD;  
DR WPI; 99-070155/06.  
PT New modified plant sucrose binding proteins - used to develop  
PT transgenic plants which can have enhanced or decreased sucrose  
PT uptake activity in developing seeds  
PS Claim 13b; Page 37-38; 58pp: English.  
CC This sequence represents a novel sucrose binding protein, SBP2 isolated  
CC from Glycine max. This protein is used in a method resulting in the  
CC production of a modified plant sucrose binding protein (SBP) which has a  
CC modified amino acid sequence compared to a corresponding wild-type SBP,  
CC and where expression of the modified SBP in a yeast assay system confers  
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.  
CC The products of the invention can be used for producing transgenic plants  
CC which have modified sucrose uptake activity, particularly in developing  
CC seeds. Enhanced sucrose uptake activity in developing seeds may be  
CC desirable where it is an advantage to increase the carbohydrate content  
CC of the seed (e.g. where the seed is the primary plant material harvested,  
CC seeds might be desirable where the vegetative material of the plant is  
CC harvested. The SBP regulatory regions confer specific or enhanced  
CC expression in developing seeds and so may be used to express any  
CC transgene in developing seeds.  
SQ Sequence 489 AA;

Query Match 22.4%; Score 95; DB 1; Length 489;  
Best Local Similarity 36.2%; Pred. No. 1.24e+00;  
Matches 17; Conservative 11; Mismatches 13; Indels 6; Gaps 5;

DB 39 LVTCKHQCQOQR-QYTESDKRTCLQOC-DSMKOE-REKQVEETREK 82  
QY 41 LQCCVQRCERRPRYSNAR--R-CVOECRDDQOGRHNEDEEGGRGR 84

RESULT 10

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ID W62831 standard; Protein: 525 AA.
AC W62831;
DE 27-OCT-1998 (first entry)
DE Theobroma cacao antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Theobroma cacao.
PN W09827805-A1.
PD 02-JUL-1998.
PE 22-DEC-1997; AU08874.
PR 20-DEC-1996; AU-004275.
PA (RENR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PS useful for controlling microbial infestations of plants or mammals
PS Claim 1: Page 47-49; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SC Sequence 525 AA:

Query Match 20.9%; Score 89; DB 1; Length 525;
Best Local Similarity 28.9%; Pred. No. 3.82e+00;
Matches 11; Conservative 14; Mismatches 12; Indels 1; Gaps 1;

DB 86 QOCQGRCEQGGGQREQQCQCKWEQYKEQERGENH 123
OY 42 QOCVORCR-QERPRYSARCVOECRDDQOQHGRHEQEE 78

RESULT 11
ID R20181 standard; Protein: 566 AA.
AC R20181;
DE 16-APR-1992 (first entry)
DE Sequence encoded by 67 kD T. cacao protein cDNA.
KW Cocoa; flavour; vicillin; seed storage protein.
OS Theobroma cacao.
PN W09119801-A.
PD 26-DEC-1991.
PE 07-JUN-1991; G00914.
PR 11-JUN-1990; GB-013016.
PA (MRSCL) MARS UK LTD.
PI Spencer MC, Hodge R, Deakin EA, Ashton S;
DR WPI: 92-024418/03.
N-PSDB: Q20377.
PT Recombinant cocoa proteins - are responsible for flavour in cocoa
PT beans and produced in large quantities using yeast and bacterial
PT expression vectors
PS Claim 4: Fig 2; 59pp; English.
CC The inventors claim a 67 kD and 31 kD T. cacao protein, and
CC fragments, and encoding DNAs. The 47 kD and 31 kD proteins are
CC derived from the 67 kD precursor. T. cacao protein cDNA was
CC detected in a cDNA library prepared from immature cocoa beans RNA
CC using a probe based on the AA sequence of a CNR peptide common to
CC the 47 kD and 31 kD polypeptides. Homology searches revealed close
CC homologies between the 67 kD polypeptide and the vicillin, which are
CC seed storage proteins.
SQ Sequence 566 AA:

Query Match 20.9%; Score 89; DB 1; Length 566;
Best Local Similarity 28.9%; Pred. No. 3.82e+00;
Matches 11; Conservative 14; Mismatches 12; Indels 1; Gaps 1;

DB 86 QOCQGRCEQGGGQREQQCQCKWEQYKEQERGENH 123
OY 42 QOCVORCR-QERPRYSARCVOECRDDQOQHGRHEQEE 78

RESULT 12
ID W46606 standard; Protein: 450 AA.
AC W46606;
DE 30-JUN-1998 (first entry)
DE Tyrosine kinase associated protein 1.

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KW tyrosine kinase associated protein-1; TKR-1; antibody;
KW detection; binding agent; diagnosis; treatment;
KW receptor dimerisation.
OS Homo sapiens.
PH Key
FT Protein
FT 7..112 Location/Qualifiers
FT /note="domain repeated in 146-252 and 346-376"
FT 146..252
FT /note="repeated from region 7-112"
FT 346..376
FT /note="repeated from region 7-112"
FT 7..89
FT /label="GLGF domain"
FT /label="Protein-protein signalling interactions"
FT 145..229
FT /label="GLGF domain"
FT /note="Protein-protein signalling interactions"
FT 145..229
FT Domain
FT 145..229
FT W09801551-A1.
PN 15-JAN-1998.
PD 16-OCT-1996; U16510.
PR 13-JUN-1996; US-666067.
PR 13-JUN-1996; US-665037.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PI Seedorf L, Ullrich A;
DR WPI: 98-101049/09.
PT Tyrosine kinase associated protein-1 - used for the diagnosis and
PT treatment of TKA-1 related diseases
PS Claim 2: Fig 1; 61pp; English.
CC The Tyrosine kinase associated protein-1 (TKA-1) contains a stretch
CC of 106 amino acids (aa/112) which is duplicated within the
CC sequence (aa 146-252) with 65% identity, and again (aa346-176) with
CC 47% identity. A binding agent of TKA-1, able to bind to a TKA-1
CC polypeptide, or the full length TKA-1 protein can both be used in a
CC method for disrupting or promoting receptor dimerisation. They can
CC also be used to identify agents capable of interfering with the
CC interaction between them. The TKA-1 antibody can be used for the
CC detection of TKA-1. The TKA-1 protein, antibody and binding agent can
CC all be used in the diagnosis and treatment of TKA-1 related diseases and
CC conditions.
SQ Sequence 450 AA:

Query Match 20.0%; Score 85; DB 1; Length 450;
Best Local Similarity 33.3%; Pred. No. 8.02e+00;
Matches 13; Conservative 13; Mismatches 10; Indels 3; Gaps 3;

DB 398 QODGRERQ-RCERSESETERERERHERERESERARG 435
OY 49 ROERPRYSARCVOEC-RDDQOQHGRH-EQEEQGRG 85

RESULT 13
ID W59348 standard; Protein: 97 AA.
AC W59348;
DE 08-SEP-1998 (first entry)
DE Human ErbB2 extracellular domain protein fragment (aa 529-625).
KW ErbB2; epitope; monoclonal antibody; identification; apoptosis;
KW detection; treatment; disorder; tumour; benign; malignant; leukemia;
KW lymphoid malignancy; inflammation; angiogenic; immunological.
OS Homo sapiens.
PN W09817797-A1.
PD 30-APR-1998.
PE 09-OCT-1997; U18385.
PR 18-OCT-1996; US-731794.
PA (GENTX) GENENTECH INC.
PA (TEXA) UNIV TEXAS SYSTEM.
PI Fendly BM, Phillips GD, Scheuermann RH, Uhr JW;
DR WPI: 98-261493/23.
PT New anti-ErbB2 antibodies - which induce apoptosis in cells which
PT overexpress ErbB2, used to treat e.g. tumours or inflammatory,
PT angiogenic or immunologic disorders
PS Disclosure; Page 46; 72pp; English.
CC This sequence represents a fragment of the human ErbB2 extracellular
CC domain corresponding to amino acids 529-625 which is capable of binding

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CC monoclonal antibodies 4D5. This region is used in a method which  
CC identifies antibodies capable of binding to ErbB2 and induce apoptosis of  
CC a cell which overexpresses ErbB2. The antibodies can also be used to  
CC detect ErbB2 on a cell. The antibodies can be used for treating disorders  
CC such as benign or malignant tumours, (e.g. renal, liver, kidney, bladder,  
CC breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,  
CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head  
CC and neck tumours), leukemias and lymphoid malignancies, other disorders  
CC such as neuronal, glial, astrocytic, hypothalamic and other glandular  
CC macrophagal, epithelial, stromal and blastocoele disorders, and  
CC inflammatory, angiogenic and immunologic disorders.  
SQ Sequence 97 AA;

Query Match 19.8%; Score 84; DB 1; Length 97;  
Best Local Similarity 44.4%; Pred. No. 9.64e+00;  
Matches 16; Conservative 7; Mismatches 7; Indels 6; Gaps 5;  
DB 10 QECVCRVYQGLPREVNRHCLP-CHPECQONG 44  
QY 42 QOCVCRCR--QERPR-YSHAR-CVQECRD-000HG 72

RESULT 14  
ID W90340 standard; protein: 444 AA.  
AC W90340;  
DI 24-MAY-1999 (first entry)  
DE G. max truncated SBP1 protein.  
KM SBP1: sucrose binding protein; SBP2: sucrose uptake; transgenic plant;  
KW seed; carbohydrate content; soybean.  
OS Glycine max.  
PN W09853086-A1.  
PD 26-NOV-1998.  
PE 21-MAY-1997; US-047568.  
PR 22-MAY-1997; US-047568.  
PA (UNITW ) UNIV WASHINGTON STATE RES FOUND.  
PI Chao WS, Grimes HD;  
PT WPI: 99-070155/06.  
PT New modified plant sucrose binding proteins - used to develop  
PT transgenic plants which can have enhanced or decreased sucrose  
PT uptake activity in developing seeds  
PS Claim 7: Page 36-37; 58pp; English.  
CC This sequence represents a novel sucrose binding protein, SBP1 isolated  
CC from Glycine max. This protein is used in a method resulting in the  
CC production of a modified plant sucrose binding protein (SBP) which has a  
CC modified amino acid sequence compared to a corresponding wild-type SBP,  
CC and where expression of the modified SBP in a yeast assay system confers  
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.  
CC The products of the invention can be used for producing transgenic plants  
CC which have modified sucrose uptake activity, particularly in developing  
CC seeds. Enhanced sucrose uptake activity in developing seeds may be  
CC desirable where it is an advantage to increase the carbohydrate content  
CC of the seed (e.g. where the seed is the primary plant material harvested,  
CC such as soybean). In contrast, decreased sucrose uptake activity in  
CC seeds might be desirable where the vegetative material of the plant is  
CC harvested. The SBP regulatory regions confer specific or enhanced  
CC expression in developing seeds and so may be used to express any  
CC transgene in developing seeds.  
SQ Sequence 444 AA;

Query Match 19.8%; Score 84; DB 1; Length 444;  
Best Local Similarity 29.2%; Pred. No. 9.64e+00;  
Matches 14; Conservative 14; Mismatches 15; Indels 5; Gaps 4;

DB 40 LVTCKHQCQOQO-QYTEGDKRVCLSCDRYHRMKQERKQIOETREK 86  
QY 41 LQOCVCRQCRQERPRYSHA--R-CVQEC-RDDQOQHGRHDEEFGGR 84

RESULT 15  
ID W90339 standard; protein: 524 AA.  
AC W90339;  
DI 24-MAY-1999 (first entry)  
DE G. max SBP1 protein.

KW SBP1: sucrose binding protein; SBP2: sucrose uptake; transgenic plant;  
KM seed; carbohydrate content; soybean.  
OS Glycine max.  
PN W09853086-A1.  
PD 26-NOV-1998.  
PE 21-MAY-1997; US-047568.  
PR 22-MAY-1997; US-047568.  
PA (UNITW ) UNIV WASHINGTON STATE RES FOUND.  
PI Chao WS, Grimes HD;  
PT WPI: 99-070155/06.  
PT New modified plant sucrose binding proteins - used to develop  
PT transgenic plants which can have enhanced or decreased sucrose  
PT uptake activity in developing seeds  
PS Disclosure; Page 34-36; 58pp; English.  
CC This sequence represents a novel sucrose binding protein, SBP1 isolated  
CC from Glycine max. This protein is used in a method resulting in the  
CC production of a modified plant sucrose binding protein (SBP) which has a  
CC modified amino acid sequence compared to a corresponding wild-type SBP,  
CC and where expression of the modified SBP in a yeast assay system confers  
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.  
CC The products of the invention can be used for producing transgenic plants  
CC which have modified sucrose uptake activity, particularly in developing  
CC seeds. Enhanced sucrose uptake activity in developing seeds may be  
CC desirable where it is an advantage to increase the carbohydrate content  
CC of the seed (e.g. where the seed is the primary plant material harvested,  
CC such as soybean). In contrast, decreased sucrose uptake activity in  
CC seeds might be desirable where the vegetative material of the plant is  
CC harvested. The SBP regulatory regions confer specific or enhanced  
CC expression in developing seeds and so may be used to express any  
CC transgene in developing seeds.  
SQ Sequence 524 AA;

Query Match 19.8%; Score 84; DB 1; Length 524;  
Best Local Similarity 29.2%; Pred. No. 9.64e+00;  
Matches 14; Conservative 14; Mismatches 15; Indels 5; Gaps 4;

DB 40 LVTCKHQCQOQO-QYTEGDKRVCLSCDRYHRMKQERKQIOETREK 86  
QY 41 LQOCVCRQCRQERPRYSHA--R-CVQEC-RDDQOQHGRHDEEFGGR 84

Search completed: Sat May 13 09:00:01 2000  
Job time : 8 secs.

